

Fri Feb 24 15:48:36 2006

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 15:16:53; Search time 567 Seconds
(without alignments)
87.743 Million cell updates/sec

Title: CHEN-554-SBQ1

Perfect score: 186

Sequence: 1 VGVAPGVGVAPGVGVAPGVGVAPGVGVAPGV 36

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Pending Patents AA Main:

- 1: /cgn2_6/ptodata/1/paa/PCTUS COMB pep.*
- 2: /cgn2_6/ptodata/1/paa/US066 COMB pep.*
- 3: /cgn2_6/ptodata/1/paa/US073 COMB pep.*
- 4: /cgn2_6/ptodata/1/paa/US074 COMB pep.*
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- 16: /cgn2_6/ptodata/1/paa/US086 COMB pep.*
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- 29: /cgn2_6/ptodata/1/paa/US099 COMB pep.*
- 30: /cgn2_6/ptodata/1/paa/US100 COMB pep.*
- 31: /cgn2_6/ptodata/1/paa/US101 COMB pep.*
- 32: /cgn2_6/ptodata/1/paa/US102 COMB pep.*
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chen-554-seq1.rapm

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- 45: /cgn2_6/ptodata/1/paa/US601 COMB pep.*
- 46: /cgn2_6/ptodata/1/paa/US602 COMB pep.*
- 47: /cgn2_6/ptodata/1/paa/US603 COMB pep.*
- 48: /cgn2_6/ptodata/1/paa/US604 COMB pep.*
- 49: /cgn2_6/ptodata/1/paa/US605 COMB pep.*
- 50: /cgn2_6/ptodata/1/paa/US606 COMB pep.*
- 51: /cgn2_6/ptodata/1/paa/US607 COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	186	100.0	148	1	PCT-US99-04440-14	Sequence 14, Appl
2	186	100.0	148	22	US-09-258-723-14	Sequence 14, Appl
3	186	100.0	148	28	US-09-841-321A-14	Sequence 14, Appl
4	186	100.0	745	1	PCT-US99-04440-38	Sequence 38, Appl
5	186	100.0	745	22	US-09-258-723-38	Sequence 38, Appl
6	186	100.0	745	28	US-09-841-321A-38	Sequence 38, Appl
7	183	98.4	42	25	US-09-554-996-2	Sequence 2, Appl
8	183	98.4	472	26	US-09-611-523-212	Sequence 212, Appl
9	183	98.4	472	33	US-10-305-278-212	Sequence 212, Appl
10	183	98.4	515	27	US-09-743-818-71	Sequence 71, Appl
11	183	98.4	515	27	US-09-743-818A-71	Sequence 71, Appl
12	183	98.4	570	37	US-10-760-320A-3032	Sequence 3032, Ap
13	183	98.4	570	37	US-10-760-620A-3032	Sequence 3032, Ap
14	183	98.4	571	27	US-09-743-818-7	Sequence 7, Appl
15	183	98.4	571	27	US-09-743-818A-7	Sequence 7, Appl
16	183	98.4	617	40	US-11-072-512-2915	Sequence 2915, Ap
17	183	98.4	660	24	US-09-463-091-5	Sequence 5, Appl
18	183	98.4	660	27	US-09-743-818-6	Sequence 6, Appl
19	183	98.4	661	27	US-09-743-818A-6	Sequence 6, Appl
20	183	98.4	692	1	PCT-US02-24483-40	Sequence 40, Appl
21	183	98.4	692	32	US-10-210-172-40	Sequence 40, Appl
22	183	98.4	698	24	US-09-463-091-3	Sequence 3, Appl
23	183	98.4	698	24	US-09-743-818-5	Sequence 5, Appl
24	183	98.4	698	27	US-09-743-818A-5	Sequence 5, Appl
25	183	98.4	698	40	US-11-053-710A-3	Sequence 3, Appl
26	183	98.4	702	31	US-10-170-205E-18017	Sequence 18017, A
27	183	98.4	702	48	US-60-453-050-10290	Sequence 10290, A
28	183	98.4	702	48	US-60-453-135-10290	Sequence 10290, A
29	183	98.4	702	48	US-60-466-412-10290	Sequence 10290, A
30	183	98.4	702	48	US-60-487-610-1797	Sequence 1797, Ap
31	183	98.4	702	49	US-60-582-609-1797	Sequence 1797, Ap
32	183	98.4	711	1	PCT-US02-24483-38	Sequence 38, Appl
33	183	98.4	711	32	US-10-210-172-38	Sequence 38, Appl
34	183	98.4	712	25	US-09-554-996-3	Sequence 3, Appl
35	183	98.4	730	1	PCT-US03-38193-2566	Sequence 2566, Ap
36	183	98.4	730	35	US-09-554-996-8	Sequence 8, Appl
37	183	98.4	730	37	US-10-723-860-2566	Sequence 2566, Ap
38	183	98.4	731	27	US-09-743-818-4	Sequence 4, Appl
39	183	98.4	731	24	US-09-463-091-2	Sequence 2, Appl
40	183	98.4	733	27	US-09-743-818A-4	Sequence 4, Appl
41	183	98.4	733	40	US-11-053-710A-2	Sequence 2, Appl
42	183	98.4	757	1	PCT-US03-09391-2	Sequence 2, Appl
43	183	98.4	757	1	PCT-US05-01773-29	Sequence 29, Appl
44	183	98.4	757	29	US-09-949-003C-1924	Sequence 1924, Ap
45	183	98.4				

ALIGNMENTS

RESULT 1
PCT-US99-04440-14
; Sequence 14, Application PC/TUS9904440
; GENERAL INFORMATION:
; APPLICANT: Urry, Dan W.

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OM protein - protein search, using sw model

Run on: February 18, 2006, 12:15:56 ; Search time 12.2546 Seconds
(without alignments)
1432.015 Million cell updates/sec

Title: US-09-554-996-2
Perfect score: 217
Sequence: 1 VGVAPGVGVAPGVGVAPGVG.....PGVGVAPGVGVAPGVGVAPG 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217	100.0	617	4	US-10-104-047-2915
2	217	100.0	660	6	US-11-053-710A-5
3	217	100.0	692	4	US-10-210-172-40
4	217	100.0	698	6	US-11-053-710A-3
5	217	100.0	711	4	US-10-210-172-38
6	217	100.0	730	3	US-09-961-403-8
7	217	100.0	733	6	US-10-723-860-2566
8	217	100.0	733	6	US-11-053-710A-2
9	217	100.0	757	5	US-10-287-436A-402
10	217	100.0	757	5	US-10-287-436A-1101
11	217	100.0	757	6	US-11-040-130-29
12	217	100.0	788	5	US-10-852-065-4
13	217	100.0	788	5	US-10-852-065-4
14	214	98.6	148	3	US-09-837-969A-14
15	214	98.6	148	3	US-09-841-321A-14
16	214	98.6	745	3	US-09-837-969A-38
17	214	98.6	745	3	US-09-841-321A-38
18	211	97.2	117	3	US-09-964-662-9
19	211	97.2	118	3	US-09-964-662-11
20	211	97.2	199	3	US-09-964-662-11
21	211	97.2	200	3	US-09-964-662-2
22	211	97.2	731	3	US-09-964-662-1
23	186	85.7	1169	2	US-08-806-029-33
24	181	83.4	119	3	US-09-807-742-15
25	133	61.3	663	4	US-10-108-260A-2477
26	123	56.7	65	4	US-10-117-931-9
27	113	52.1	111	3	US-09-837-969A-13

28	113	52.1	111	3	US-09-837-969A-58	Sequence 58, Appl
29	113	52.1	111	3	US-09-841-321A-13	Sequence 13, Appl
30	113	52.1	111	3	US-09-841-321A-58	Sequence 58, Appl
31	113	52.1	782	3	US-09-837-969A-37	Sequence 37, Appl
32	113	52.1	782	3	US-09-841-321A-37	Sequence 37, Appl
33	113	52.1	832	2	US-08-806-029-27	Sequence 27, Appl
34	113	52.1	936	2	US-08-806-029-26	Sequence 26, Appl
35	113	52.1	972	2	US-08-806-029-30	Sequence 30, Appl
36	113	52.1	988	2	US-08-806-029-28	Sequence 28, Appl
37	113	52.1	1024	2	US-08-806-029-31	Sequence 31, Appl
38	113	52.1	1040	2	US-08-806-029-32	Sequence 32, Appl
39	113	52.1	1056	2	US-08-806-029-29	Sequence 29, Appl
40	113	52.1	2003	3	US-09-837-969A-34	Sequence 34, Appl
41	113	52.1	2003	3	US-09-841-321A-34	Sequence 34, Appl
42	112.5	51.8	40	4	US-10-096-986-43	Sequence 43, Appl
43	112.5	51.8	50	3	US-09-837-969A-29	Sequence 29, Appl
44	112.5	51.8	50	3	US-09-841-321A-29	Sequence 29, Appl
45	112.5	51.8	50	5	US-10-797-606-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-104-047-2915
; Sequence 2915, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2915

Query Match 100.0%; Score 217; DB 4; Length 617;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPG 42
Db	388	VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPG 429

RESULT 2
US-11-053-710A-5
; Sequence 5, Application US/11053710A
; Publication No. US20050204408A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, ANTHONY S
UNIVERSITY, SYDNEY
; TITLE OF INVENTION: TROPOELASTIN DERIVATIVES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
ADDRESSEE: GRIFFITH HACK
STREET: 168 WALKER STREET
CITY: NORTH SYDNEY
STATE: NEW SOUTH WALES
COUNTRY: AUSTRALIA
ZIP: 2060
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC?DOS/MS?DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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OM protein - protein search, using sw model

Run on: February 18, 2006, 12:15:56 ; Search time 207.745 Seconds
(without alignments)
1432.015 Million cell updates/sec

Title: US-09-554-996-3

Perfect score: 3677

Sequence: 1 MAGLTAAPRPGVLLLSI.....LSPIFGAGLKGKGRK 712

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:**
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:**
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:**
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:**
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:**
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3652	99.3	730	3	US-09-961-403-8
2	3652	99.3	730	5	US-10-723-860-2566
3	3616.5	98.4	711	4	US-10-210-172-38
4	3586.5	97.5	757	5	US-10-287-436A-402
5	3586.5	97.5	757	6	US-10-287-436A-1101
6	3586.5	97.5	757	6	US-11-040-130-29
7	3561	96.8	788	5	US-10-852-065-4
8	3561	96.8	788	5	US-10-852-575-3
9	3485	94.8	698	6	US-11-053-710A-3
10	3458.5	94.1	731	3	US-09-964-662-1
11	3458.5	94.1	733	6	US-11-053-710A-2
12	3416	92.9	692	4	US-10-210-172-40
13	3244.5	88.2	663	4	US-10-108-260A-2477
14	3118.5	84.8	660	6	US-11-053-710A-5
15	3095.5	84.2	617	4	US-10-104-047-2915
16	1150	31.3	988	2	US-08-806-029-28
17	1148.5	31.2	965	4	US-10-800-179-31
18	1148.5	31.2	965	5	US-10-845-775A-31
19	1148.5	31.2	965	5	US-10-845-936A-31
20	1148.5	31.2	965	5	US-10-939-036-31
21	1136.5	30.9	1038	4	US-10-800-179-30
22	1136.5	30.9	1038	5	US-10-845-775A-30
23	1136.5	30.9	1038	5	US-10-845-936A-30
24	1136.5	30.9	1038	5	US-10-939-036-30
25	1135	30.9	832	2	US-08-806-029-27
26	1133.5	30.8	889	2	US-08-806-029-19
27	1133.5	30.8	936	2	US-08-806-029-26

ALIGNMENTS

RESULT 1

US-09-961-403-8
; Sequence 8, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-8

Query Match	99.3%	Score 3652;	DB 3;	Length 730;
Best Local Similarity	97.4%	Pred. No. 1.2e-192;		
Matches 711;	Conservative 0;	Mismatches 1;	Indels 18;	Gaps 1;
Qy	1	MAGLTAAPRPGVLLLSILHPSRPGGVGPAIPGGVPGGVPGAGLGGALGPGG	60	
Db	1	MAGLTAAPRPGVLLLSILHPSRPGGVGPAIPGGVPGGVPGAGLGGALGPGG	60	
Qy	61	KPLKVPDGGLAGLGGAGLGAFAVTPFGALVPGGVADAAAAYAAKAGAGLGGVPGVG	120	
Db	61	KPLKVPDGGLAGLGGAGLGAFAVTPFGALVPGGVADAAAAYAAKAGAGLGGVPGVG	120	
Qy	121	LGVSAAGVPPQAGVKKVPGVGLPGVPGVPGVLPGARPPGVLPQVPTGAGVKPAP	180	
Db	121	LGVSAAGVPPQAGVKKVPGVGLPGVPGVPGVLPGARPPGVLPQVPTGAGVKPAP	180	
Qy	181	GVGAGFAGIPGVPGFPGQVPLGYPIKAPKPLGGYGLPYTTGKLPYGYGPGGVAGAAG	240	
Db	181	GVGAGFAGIPGVPGFPGQVPLGYPIKAPKPLGGYGLPYTTGKLPYGYGPGGVAGAAG	240	
Qy	241	KAGYPTGTGTGVPQAAAAAAYAAKAFGAGAGVLPVGGVAGVPGVPGAIPIGIGIAGVT	300	
Db	241	KAGYPTGTGTGVPQAAAAAAYAAKAFGAGAGVLPVGGVAGVPGVPGAIPIGIGIAGVT	300	
Qy	301	PARAAAAAAYAAKAFGAGAGVLPVGGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPG	360	